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# UniProtKB/TrEMBL entry O75807

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## Entry information

Entry name	O75807_HUMAN
Primary accession number	O75807
Secondary accession numbers	None
Entered in TrEMBL in	Release 08, November 1998
Sequence was last modified in	Release 08, November 1998
Annotations were last modified in	Release 30, May 2005
<b>Name and origin of the protein</b>	
Protein name	<b>Apoptosis associated protein</b>
Synonym	<b>Protein phosphatase 1, regulatory subunit 15A</b>
Gene name	<b>Name: PPP1R15A</b>
From	Synonyms: GADD34
Taxonomy	Homo sapiens (Human) [TaxID: 9606] Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

## References

### [1] NUCLEOTIDE SEQUENCE.

DOI=10.1074/jbc.272.21.13731; PubMed=9153226 [NCBI, ExPASy, EBI, Israel, Japan]  
 Hollander M.C., Zhan Q., Bae I., Fornace A.J. Jr.;  
 "Mammalian GADD34, an apoptosis- and DNA damage-inducible gene.";  
 J. Biol. Chem. 272:13731-13737(1997).

### [2] NUCLEOTIDE SEQUENCE.

**TISSUE**=Brain;  
 DOI=10.1073/pnas.242603899; PubMed=12477932 [NCBI, ExPASy, EBI, Israel, Japan]  
 Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L.,  
 Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Marra M.A.;  
 "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA  
 sequences.";  
 Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

### [3] NUCLEOTIDE SEQUENCE.

**TISSUE**=Brain;  
 Strausberg R.;  
 Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.

## Comments

None

**Cross-references****Sequence databases**

EMBL U83981; AAC25631.1; -; mRNA. [EMBL / GenBank / DDBJ] [CoCodingSequence]  
BC003067; AAH03067.1; -; mRNA. [EMBL / GenBank / DDBJ] [CoCodingSequence]

**3D structure databases**

ModBase O75807.

**2D gel databases**

SWISS-2DPAGE Get region on 2D PAGE.

**Organism-specific gene databases**

Ensembl ENSG00000087074; Homo sapiens. [Contig view]

HGNC HGNC:14375; PPP1R15A.

GeneCards PPP1R15A.

GeneLynx PPP1R15A; Homo sapiens.

GenAtlas PPP1R15A.

HOVERGEN [Family / Alignment / Tree]

**Gene expression databases**

CleanEx HGNC:14375; PPP1R15A.

**Ontologies**

GO:0006915; Biological process: apoptosis (traceable author statement).

GO:0007050; Biological process: cell cycle arrest (traceable author statement).

GO GO:0006974; Biological process: response to DNA damage stimulus (traceable author statement).

QuickGo  
view.

**Family and domain databases**

ProDom [Domain structure / List of seq. sharing at least 1 domain]

**Other**

ProtoMap O75807.

PRESAGE O75807.

UniRef View cluster of proteins with at least 50% / 90% / 100% identity.

**Keywords**

None

**Features**

None

**Sequence information**

Length: 674 Molecular weight: 73478 CRC64: B257AA17456D1403 [This is a checksum on the  
AA Da sequence]

10	20	30	40	50	60
MAPGQAPHQA	TPWRDAHPFF	LLSPVMGLLS	RAWSRLRGLG	PLEPWLVEAV	KGAALVEAGL
70	80	90	100	110	120
EGEARTPLAI	PHTPWGRRPE	EEAEDSGGPG	EDRETLGLKT	SSSLPEAWGL	LDDDDGMYGE
130	140	150	160	170	180
REATSVPRGQ	GSQFADGQRA	PLSPSLLIRT	LQGSDKNPGE	EKAEEEGVAE	EEGVNKFSYP

190 200 210 220 230 240  
 PSHRECCPAV EEEEDDEEAVK KEAHRTSTSA LSPGSKPSTW VSCPGEEENQ ATEDKRTERS  
 250 260 270 280 290 300  
 KGARKTSVSP RSSGSDPRS W EYRSGEASEE KEEKAHKETG KGEAAPGPQS SAPAQRPQLK  
 310 320 330 340 350 360  
 SWWCQPSDEE EGEVKALGAA EKDGEAECP P CIPPPSAFLK AWVYWPGE DT EEEEDEEEDE  
 370 380 390 400 410 420  
 DSDSGSDEEE GEAEASSSTP ATGVFLKSWV YQPGEDTEEE EDEDSDTGSA EDEREAETSA  
 430 440 450 460 470 480  
 STPPASAFLK AWVYRPGE DT EEEEDEDVDS EDKEDDSEAA LGEAESDPHP SHPDQRAHFR  
 490 500 510 520 530 540  
 GWGYRPGKET EEEEAAEDWG EAEP CPFRVA IYVPGEKPPP PWAPPRLPLR LQRRLKRPET  
 550 560 570 580 590 600  
 PTHDPDPETP LKARKVRFSE KVTVHFLAVW AGPAQAARQG PWEQLARDRS RFARRITQAQ  
 610 620 630 640 650 660  
 EELSPCLTPA ARARAWARLR NPPLAPIPAL TQTLPSVSSVP SSPVQTTPLS QAVATPSRSS  
 670  
 AAAAAALDLS GRRG

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FASTA  
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or at NCBI (USA)



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Compute pI/Mw, PeptideMass, PeptideCutter,  
Dotlet (Java)

 ScanProsite, MotifScan



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**NPS@** NPSA Sequence analysis  
tools

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